Claims

1. A method for identifying a candidate compound for treating, reducing, or preventing a pathogenic infection, said method comprising:

(a) contacting a pathogenic cell with a candidate compound; and

(b) measuring the production of a molecule selected from the group consisting of an 4-hydroxy-2-alkylquinoline (HAQ) molecule, 4-hydroxy-2-heptylquinoline (HHQ) molecule, or a derivative or precursor thereof in said cell, a candidate compound that reduces said production relative to production of said molecule by a cell not contacted with said candidate compound, identifying a candidate compound useful for treating, reducing, or preventing a pathogenic infection.

2. The method of claim 1, wherein step (b) comprises measuring the HAQ molecule.

3. The method of claim 1, wherein said pathogenic cell infects a mammal.

4. The method of claim 3, wherein said mammal is a human.

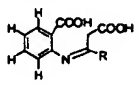
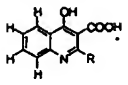
5. The method of claim 1, wherein said pathogenic cell infects a plant.

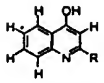
6. The method of claim 1, wherein said pathogenic cell is *Pseudomonas aeruginosa*.

7. The method of claim 6, wherein said *Pseudomonas aeruginosa* PA14 or PA01.

8. The method of claim 1, wherein said HAQ molecule, said HHQ molecule, or said derivative or precursor thereof is selected from any one of the molecules shown in Fig. 5 or Fig. 2.

9. The method of claim 8, wherein said molecule is selected from the group consisting of

 and 

10. The method of claim 1, wherein said HHQ is 

11. A method for identifying a candidate compound for treating, reducing, or preventing a pathogenic infection, said method comprising:

(a) contacting a population of cultured pathogenic cells with a candidate compound;

(b) collecting supernatant from said population of cultured pathogenic cells;

(c) contacting said collected supernatant with a second population of cells expressing a PqsH protein;

(d) measuring production of HHQ in said population of cells, a candidate compound that reduces said production relative to HHQ production in a population of cells contacted with supernatant collected from a population of cells that has not been contacted with said candidate compound, identifying a candidate compound useful for treating, reducing, or preventing a pathogenic infection.

12. The method of claim 11, wherein said pathogenic cells infect mammals.

13. The method of claim 12, wherein said mammal is a human.

14. The method of claim 11, wherein said pathogenic cells infect plants.

15. The method of claim 11, wherein said pathogenic cells are *Pseudomonas aeruginosa*.

16. The method of claim 15, wherein said *Pseudomonas aeruginosa* are *Pseudomonas aeruginosa* PA14 or *Pseudomonas aeruginosa* PAO1.

17. The method of claim 11, wherein said PqsH protein is encoded by a nucleic acid molecule substantially identical to the nucleic acid of SEQ ID NO:6 or by a nucleic acid molecule that binds under stringent conditions to SEQ ID NO:6 or a sequence complementary thereto.

18. The method of claim 11, wherein said PqsH protein is substantially identical to the amino acid sequence of SEQ ID NO:13.

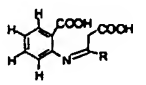
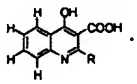
19. The method of claim 11, wherein said PqsH protein is a *Pseudomonas aeruginosa* PqsH protein.

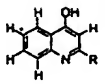
20. A method for identifying a candidate compound for treating, reducing, or preventing a pathogenic infection, said method comprising:

(a) contacting a molecule selected from the group consisting of an HAQ molecule, an HHQ molecule, a precursor thereof, or a derivative thereof with a candidate compound; and

(b) determining whether said candidate compound binds said molecule, a candidate compound that binds to and decreases the activity of said molecule being a candidate compound useful for treating, reducing, or preventing a pathogenic infection.

21. The method of claim 21, wherein said molecule is selected from the group consisting of any one of the molecules shown in Fig. 2, Fig. 5,

 , and  .

22. The method of claim 20, wherein said HHQ is 

23. A method of identifying a candidate compound for treating, reducing, or preventing a pathogenic infection, said method comprising:

(a) contacting a candidate compound; a Pqs protein, and a molecule selected from the group consisting of an HAQ molecule, a derivative or precursor thereof, wherein said molecule is capable of binding said Pqs protein under conditions that allow binding; and

(b) measuring the binding of said Pqs protein to said molecule, wherein a decrease in said binding effected by said candidate compound identifies a candidate compound useful for treating, reducing, or preventing a pathogenic infection.

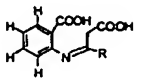
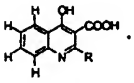
24. The method of claim 23, wherein said Pqs protein is selected from the group consisting of pqsA, pqsB, pqsC, pqsD, pqsE, pqsH, and pqsL protein.

25. The method of claim 24, wherein said Pqs protein comprises an amino acid sequence substantially identical to any one of SEQ ID NOs:8-14.

26. The method of claim 25, wherein said Pqs protein is encoded by a nucleic acid molecule that is substantially identical to or that hybridizes under stringent conditions to any one of SEQ ID NOs:1-7.

27. The method of claim 23, wherein said Pqs protein is a *Pseudomonas aeruginosa* Pqs protein.

28. The method of claim 23, wherein said molecule is selected from the group consisting of any one of the molecules shown in Fig. 2, Fig. 5,

 , and  .

29. A method of identifying a candidate compound for treating, reducing, or preventing a pathogenic infection, said method comprising:

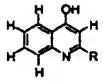
(a) contacting a candidate compound; a PqsH protein, and an HHQ molecule capable of binding said PqsH protein under conditions that allow binding; and

(b) measuring the binding of said PqsH protein to said HHQ molecule, wherein a decrease in said binding effected by said candidate compound identifies a candidate compound useful for treating, reducing, or preventing a pathogenic infection.

30. The method of claim 29, wherein said PqsH protein comprises an amino acid sequence substantially identical to SEQ ID NO:13.

31. The method of claim 29, wherein said PqsH protein is encoded by a nucleic acid molecule that is substantially identical to or that hybridizes under stringent conditions to SEQ ID NO:6.

32. The method of claim 29, wherein said PqsH protein is a *Pseudomonas aeruginosa* PqsH protein.

33. The method of claim 29, wherein said HQQ molecule is wherein said HHQ is  .

34. A method of identifying a candidate compound for treating, reducing, or preventing a pathogenic infection, said method comprising:

(a) contacting a candidate compound; an MvfR protein, and a nucleic acid molecule substantially identical to the nucleic acid of SEQ ID NO:15 or with a nucleic acid molecule that binds under stringent conditions to SEQ ID NO:15 or a sequence complementary thereto or fragment thereof,

(b) measuring the binding of said MvfR protein to said nucleic acid molecule, wherein a decrease in said binding effected by said candidate compound identifies a candidate compound useful for treating, reducing, or preventing a pathogenic infection.

35. The method of claim 34, wherein said MvfR protein comprises an amino acid sequence substantially identical to SEQ ID NO:17.

36. The method of claim 34, wherein said MvfR protein is encoded by a nucleic acid molecule that is substantially identical to or that hybridizes under stringent conditions to SEQ ID NOs:16.

37. The method of claim 34, wherein said MvfR protein is a *Pseudomonas aeruginosa* MvfR protein.

38. The method of claim 34, wherein said fragment includes the *lysR-box* sequence.

39. A method of identifying a candidate compound for treating, reducing, or preventing a pathogenic infection, said method comprising:

(a) contacting a cell containing a *pqs*-reporter with a candidate compound and a PQS molecule; and

(b) measuring the induction of the reporter, wherein a decrease in said reporter gene activity relative to an untreated cell identifies a candidate compound useful for treating, reducing, or preventing a pathogenic infection.

40. The method of claim 39, wherein said cell is a *pqsA* strain.

41. The method of claim 40, wherein said reporter is the *pqsA-LacZ* reporter gene.

42. The method of claim 39, wherein said cell infects a mammal.

43. The method of claim 42, wherein said mammal is a human.

44. The method of claim 39, wherein said cell infects a plant.

45. The method of claim 44, wherein said cell is *Pseudomonas aeruginosa*.

46. The method of claim 45, wherein said *Pseudomonas aeruginosa* PA14 or PA01.

47. A method of identifying a candidate compound for treating, reducing, or preventing a pathogenic infection, said method comprising:

(a) contacting a nucleic acid molecule substantially identical to the nucleic acid of SEQ ID NO:15 or with a nucleic acid molecule that binds under stringent conditions to SEQ ID NO:15 or a sequence complementary thereto or fragment thereof with a candidate compound,

(b) determining whether said candidate compound binds said nucleic acid molecule, a candidate compound that binds to said nucleic acid molecule being a candidate compound useful for treating, reducing, or preventing a pathogenic infection..

48. The method of claim 47, wherein said fragment includes the *lysR-box* sequence.

49. The method of any one of claims 1, 11, 20, 23, 29, 34, 39, and 47 wherein said candidate compound is immobilized on a support.

50. The method of any one of claims 1, 11, 20, 23, 29, 34, 39, and 47, wherein said candidate compound has a detectable group.

51. The method of any one of claims 1, 11, 20, 23, 29, 34, 39, and 47, wherein said candidate compound is expressed on the surface of a phage.

52. The method of any one of claims 1, 11, 20, 23, 29, 34, 39, and 47, wherein said candidate compound is expressed using RNA display.

53. The method of any one of claims 1, 11, 20, 23, 29, 34, 39, and 47, wherein said candidate compound inhibits the virulence of a pathogen.

54. The method of any one of claims 20, 23, 29, 34, and 47, wherein said contacting occurs in a cell free system.

55. The method of any one of claims 20, 23, 29, 34, and 47, wherein said contacting occurs in a cell.